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LAM, Toong Jin

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XU, Yanfei

HE, Jiangyan

YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF
FLUORESCENT TRANSGENIC ORNAMENTAL FISH

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<170> PatentIn Ver. 2.0

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Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr

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Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr

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Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly
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Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Asn Leu Leu
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Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Ala Val Arg Thr Ser
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Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile
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Asp Lys Val Arg Phe Leu Glu Asn Lys Met Leu Glu Thr Lys Trp Ser
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Leu Leu Glu Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala
145 150 155 160
Tyr Ile Ser Asn Leu Arg Arg Leu Asp Gly Leu Gly Asn Glu Lys Met
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Lys Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe
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Glu Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys
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Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asp Glu Ile Asn Phe Leu
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Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Ile Lys Asp
245 250 255
Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met Asp
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Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn Arg
275 280 285
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Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu
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Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Asn Glu Ile Asp Ala
325 330 335
Val Lys Ala Arg Ala Asn Leu Glu Ala Gln Ile Ala Glu Ala Glu Glu
340 345 350
Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg Ile Arg Glu Leu
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370 375 380
Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu Asp Ile Glu Ile Ala

385 390 395 400
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 420 425 430
 Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser
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 Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys
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cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208
 His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys

30 35 40

ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256
 Leu Arg Asp Lys Gln Thr Pro Pro Gly Phe Thr Val Asp Asp Val Ile

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cag act ggt gtt gac aat cca ggc cac ccc ttc atc atg acc gtc ggc 304
 Gln Thr Gly Val Asp Asn Pro Gly His Pro Phe Ile Met Thr Val Gly

60 65 70

tgt gtt gct ggt gat gag gag tcc tac gat gtt ttc aag gac ctg ttc 352
 Cys Val Ala Gly Asp Glu Glu Ser Tyr Asp Val Phe Lys Asp Leu Phe

75 80 85

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cac aag acc gac ctc aac ttt gag aac ctg aag ggt ggt gat gac ctg 448
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Lys Gly Tyr Pro Leu Pro Pro His Asn Ser Arg Gly Glu Arg Arg Ala
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Val Glu Lys Leu Ser Val Glu Ala Leu Ser Ser Leu Asp Gly Glu Phe
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170 175 180 185
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205 210 215
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Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp
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cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg 832
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 Pro Ala Gln Lys
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 Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
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 Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
 65 70 75 80
 Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg
 85 90 95
 His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe
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 Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser
 115 120 125
 Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro
 130 135 140
 His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu
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 Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu
 165 170 175
 Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe
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 Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met
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 Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly
 245 250 255

Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met
 260 265 270
 Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly
 275 280 285
 Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr
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 His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg
 305 310 315 320
 Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile
 325 330 335
 Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys
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 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
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 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
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35 40 45

Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala

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Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro

65 70 75 80

His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr

85 90 95

Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg

100 105 110

Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr

115 120 125

Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr

130 135 140

Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu

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Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn

165 170 175

Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile

180 185 190

Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp

195 200 205

Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn

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225 230 235 240

Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val

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Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr

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<223> CK2
<220>
<221> misc feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA
<400> 7

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tcacacctgg ttatactat gatagttgta cagtgtggtc tgtgacaccc aactgtgccc 120
aattgtctga ctatgcaggg tgtctatgcg tatagtttac agttagacca aagtgtgctg 180
gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240
tagtgcagtg ttgtacttt tatttcaatt ttattctgt ctatgtggat tagacaaatc 300
acatagaagg taaatcacat cataatgaac agcaaactgt ttgccagcat taaaagaaga 360
agactgctta gatgcatgtc actgatgaga aaataacttt aaacgcacac aagacggcac 420
gtacccaac gcagtgggga cgttgcaatt gaactcaacg tcaggtcgat gtcaatgttc 480
ctaataatgt tacagcttga tgttatgcgg ggattatggt tgccatacct gatgaataaa 540
gggtgcacat tggattttgg tcgctttcca cctatgacat cgttattgga cgtcaaaaata 600
aatttaggtc accacaacct atatttaacc tgcctgggcaa taactaaatg cactacagaa 660
taaataatgc agcttttacc agcataatac aaaagctact ttactcat actttgagta 720
acatttttag gcatgtattg atattttac cagccctccc catacataat cgtatgttta 780
acattagctt ttttagccgc tagcattact gagcttgtgc atgaaagcag atttgagct 840
gatgattgcc gtaccatgat ctacacctt gacgattgag taatgtctatt aaatgcccat 900
attcgtgtt gactgcacg agaaatgaga tgggaacatt tatcagtggc cattaaatac 960
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aagacgtcaa catggcgta ggttgacgtt tgttagaaa tgaaaattag gttgacgtca 1260
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caacatttat ctaccactt tctctctga cctgtctaac aggtaggtgtg tgtgtgagag 2040
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actcaaagac acaggatccg g
2241

<210> 8

<211> 1456
<212> DNA
<213> Danio rerio
<220>
<221> TATA signal
<222> (1389)..(1394)
<220>
<221> primer bind
<222> (1433)..(1456)
<223> MCK2
<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA
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gcatgtgcac catgacaggc ctgttattca cacttgggtgc catgttggag actgttcggc 180
cagctatagt ttcttcaca gagtctggg tcacctaag tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgtag tgcattact aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg gggtttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt ctttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtaaatgg gtctccagc atttttcaa tataccttac ttgagttca aaagaaaaac 660
acatctcaaa taggtttgag gttgaataaa cattttcat ttgggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaat cattttatag actttctccc ctattaaac 780
atggttgaat ttatctcat gtttatgtct ggggtgtgct ttttgaaaa gatttcctg 840
tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gcccttcac cctcagtga taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgcac 1020
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cagatctccc acatcccatc accctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
catctaggat gccctggggc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttacgtgagc tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgctg ggtgaccctt attcggctt 1440
ggtgaacagg atccgg

1456

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio
<220>
<221> primer bind
<222> (2179)..(2205)
<223> ARP2
<220>
<221> misc_feature

<222> (2153)..(2199)

<223> Identical to the 5' ARP cDNA

<220>

<221> intron

<222> (792)..(2152)

<220>

<221> misc_feature

<222> (775)..(791)

<223> Identical to the 5' ARP cDNA

<400> 9

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agaaataata caaatttgtt tacagtattc ttagtatttg caataaacga attttatata 180
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgactttt tgggcggacc aaattccctt attaatggc aattcattaa 360
aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggctgttg ttgaaggga tacatctgcg gccgaaagt aacgggaact 480
atttacattc ttgtctatta aattatccat tattgtatt ttattacccc aaccgtaaac 540
tcaacctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatgc 600
tatattgacc gcagctgtat ctttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgaca gatacgcat tccgcgcga ttctgattgg 720
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aagatgcaca caaggcagggt gtaaaagtat tgcttgtgtt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gtcaccgat ccttgaagg gatcc 2205

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Cytokeratin - gene specific primer
 <400> 10
 cgctggagta agagatagac ctgg 24
 <210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Cytokeratin gene specific primer
 <220>
 <221> misc feature
 <222> (1)..(6)
 <223> Introduced for restriction site
 <220>
 <221> misc feature
 <222> (3)..(8)
 <223> BamHI site
 <400> 11
 ccggatcctg tgtcttgag ttgctg 26
 <210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:
 Muscle creatine kinase gene specific primer
 <220>
 <221> misc feature
 <222> (3)..(8)
 <223> BamHI site
 <400> 12
 ccggatcctt gggatcagat cctg 24
 <210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:
 Muscle creatine kinase gene specific primer
 <220>
 <221> misc feature
 <222> (1)..(3)
 <223> Introduced for restriction site
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 <221> misc feature
 <222> (3)..(B)
 <223> BamHI site
 <400> 13

ccggatcctg ttcaccaagc cgaa 24

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<400> 14

tagttggact tccacgtgcc ctgtc 25

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<220>

<221> misc feature

<222> (1)..(7)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (1)..(6)

<223> BamHI site

<400> 15

ggatcccttc caaggatcgg tgaaca 26

<210> 16

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide for linker used in linker-mediated PCR

<400> 16

gttcacotctt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide for linker used in linker-mediated PCR

<220>

<223> n is a dideoxycytidine

<400> 17

gaattcaagn 10

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

linker specific primer

<400> 18

gttcattctt acaagctagc g 21

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

linker specific primer

<400> 19

tcctgaacaa tgctgtggac 20

<210> 20

<211> 1392

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (42)..(551)

<220>

<221> primer bind

<222> (6)..(28)

<223> M2

<220>

<221> primer bind

<222> (23)..(45)

<223> M1

<220>

<221> polyA signal

<222> (797)..(802)

<220>

<221> polyA_signal <222> (1351)..(1357)

<400> 20

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Met Ala Pro Lys Lys

1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104

Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser

10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152

Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile

25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200

Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp

40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248

Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu

55 60 65
 gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
 Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
 70 75 80 85
 acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
 Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
 90 95 100
 gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
 Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
 105 110 115
 aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
 Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
 120 125 130
 gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
 Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
 135 140 145
 ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
 Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
 150 155 160 165
 gag aag gag gag taa acaacctgg aatagaggaa acgaagagaa gaacatgcat 591
 Glu Lys Glu Glu
 170

cctcacagct taatctccag tctgtgtct ggccttctct aacttttgtt ttctctcct 651
 ccctttcttg ctttctacca tcgtgtgtac tccaagcact tacactctcc atcttaccaa 711
 agactgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771
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 aataaaaaaaa aaaaaaaaaa a 1392

<210> 21

<211> 169

<212> PRT

<213> Danio rerio

<400> 21

Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
 1 5 10 15
 Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
 20 25 30
 Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
 35 40 45
 Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
 50 55 60
 Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn

65 70 75 80
 Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
 85 90 95
 Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
 100 105 110
 Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
 115 120 125
 Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
 130 135 140
 Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
 145 150 155 160
 Ile Thr His Gly Glu Glu Lys Glu Glu
 165

<210> 22

<211> 2054

<212> DNA

<213> Danio rerio

<220>

<221> TATA signal

<222> (1983)..(1989)

<220>

<221> enhancer

<222> (142)..(148)

<223> E-box, canntg

<220>

<221> enhancer

<222> (452)..(457)

<223> E-box, canntg

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<221> enhancer

<222> (1095)..(1100)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1278)..(1283)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1362)..(1367)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1385)..(1390)

<223> E-box, canntg

<220>

<221> enhancer

<222> (523)..(532)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (606)..(615)
 <223> Potential MEF2 binding site, yta(w)4tar
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 <221> enhancer
 <222> (697)..(706)
 <223> Potential MEF2 binding site, yta(w)4tar
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 <221> enhancer
 <222> (1490)..(1499)
 <223> Potential MEF2 binding site, yta(w)4tar
 <220>
 <221> enhancer
 <222> (1640)..(1649)
 <223> Potential MEF2 binding site, yta(w)4tar
 <220>
 <221> enhancer
 <222> (1956)..(1965)
 <223> Potential MEF2 binding site, yta(w)4tar
 <220>
 <223> Transcription start site at residue 2012
 <220>
 <221> primer bind
 <222> (2032)..(2054)
 <223> M2
 <220>
 <221> misc difference
 <222> (2027)..(2054)
 <223> Identical to the 5' MLC2f cDNA
 <409> 22
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 tgttatatt gtgcataac attagattag aagctgtcac tgcggtggtc cttttcaaa 180
 ttgatactc aaaagtatat attagtgcct ttaggtact aatatatacc cttgaggttt 240
 tcatttgaa aggtaccacc ccagtgcag aaatctggag cttatttaac aaaataactt 300
 tatttatg ttattgaaaa atattaaata agcaaaacaa tggaaaaaaa ttagtcaaa 360
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 caagcaggag caaaacaagc cgacagactc gggaatgcac aacaaactca agggggggcaa 540
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 caaccactca gagggtgta gtgtgtgac cgtgctgtc cacagggcag ctcccacaa 660
 gtgaggtcat aggtcgatcg gcagagagag atgggcatgg ccatgtggac ggggtgtgtg 720
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<210> 23

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

MLC2F gene specific primer M1

<400> 23

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<220>

<223> Description of Artificial Sequence:

MLC2F gene specific primer M2

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